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Other:	Other:	

<sup>\*</sup>Examin r: The abov c rrections must be communicated to th applicant in the first Office Action. DO NOT send a copy of this form.

### RAW SEQUENCE LISTING PATENT APPLICATION US/08/779,460B

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This Raw Listing contains the General Information Section and up t the first pages.

ERED 1 SEQUENCE LISTING 2 3 General Information: (1) 5 (i) APPLICANT: Oscar Johannes Maria GODDIJN 6 Teunis Cornelis VERWOERD 7 Ronny Wilhelmus Hermanus Henrika KRUTWAGEN 8 Eline VOOGD 9 10 (ii) TITLE OF INVENTION: ENHANCED ACCUMULATION OF TREHALOSE IN PLANTS 11 12 NUMBER OF SEQUENCES: 27 13 (iii) 14 (iv) CORRESPONDENCE ADDRESS: 15 16 (A) ADDRESSEE: 17 LADAS & PARRY 18 STREET: 26 WEST 61 STREET 19 (B) 20 (C) CITY: NEW YORK 21 22 STATE: NY 23 (D) 24 25 (E) COUNTRY: USA 26 27 (F) ZIP: 10023 28 29 30 (v) COMPUTER READABLE FORM: 31 32 33 (A) MEDIUM TYPE: 3-1/4" Disk 1.44 MB 34 35 (B) COMPUTER: IBM PC Compatible 36 37 OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11 (C) 38 39 (D) SOFTWARE: WordPerfect 6.1 for Windows 40 41 (vi) CURRENT APPLICATION DATA: 42 43 (A) APPLICATION NUMBER: 08/779,460 44 (B) FILING DATE: 07-JAN-1997 45 46

PAGE: 2

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/779,460B

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50	(vii)	PRIOR APPLICATION	I DATA:		
51					
52	(A)	APPLICATION NUMBE	ER: PY000	0009/96	
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54	(B)	FILING DATE:	12-JAN-1996		
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56	(Viii)	ATTORNEY/AGENT IN	IFORMATION:		
57					
58	(A)	NAME:	MASS,	Clifford J.	
59					
60	(B)	REGISTRATION NO.:	30,086		
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72					
73	(2) INFORMATIO	N FOR SEQ ID NO: 1	. :		
74	(-,				
75	(i) SEQUENC	E CHARACTERISTICS:			
76	(A)	LENGTH: 2621 base	pairs		
77	(B)	TYPE: nucleic acid	<u></u>		
78	(C)	STRANDEDNESS: doub	ole		
79	(D)	TOPOLOGY: linear			
80					
81	(ii) MOLECU	LE TYPE: cDNA to m	RNA		
82					
83	(iii) HYPOT	HETICAL: NO			
84					
85	(ix) FEATUR				
86	• •	NAME/KEY: CDS			
87		LOCATION: 252485			
88	(D)	OTHER INFORMATION:			,
89				h. phosphatase"	
90 91		/product= "bipa	irtite enzyme"	•	
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104	Gln	Met	Leu	Pro	Asn	Arq	Lu	Ile	Val	Val	Ser	Asn	Gln	Leu	Pro	Ile	
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113				45					50					55			
114																	
115	CAG	CCG	TTG	AGG	TTT	TCT	ATT	CTT	GGC	GAT	CCA	CTA	AGG	GCT	GAC	GTT	243
116	Gln	Pro	Leu	Ara	Phe	Ser	Ile	Leu	Gly	Asp	Pro	Leu	Arg	Ala	Asp	Val	
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123												TGG					339
124	Asn	Cys	Val	Ala	Val	Phe	Val	Pro	Thr	Ser		Trp	Asp	GTN	Tyr		
125	90					95					100					105	
126																	
127	CAC	TGC	TTT	TGT	AAG	CAG	TAT	TTG	TGG	CCG	ATA	$\mathbf{T}\mathbf{T}\mathbf{T}$	CAT	TAC	AAG	GTT	387
128	His	Cys	Phe	Cys	Lys	Gln	Tyr	Leu	Trp	Pro	Ile	Phe	His	Tyr	Lys	Val	
129		-		-	110		-		_	115					120		
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131	CCC	GCT	тст	GAC	GTC	AAG	AGT	GTC	CCG	AAT	AGT	CGG	GAT	TCA	TGG	AAC	435
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137			140					145					150				
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140	Val	Thr	Asn	Arg	Ser	Asn	Tyr	Val	Trp	Ile	His	Asp	Tyr	His	Leu	Met	
141		155					160					165					
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143	ACG	CTA	CCG	ACT	TTC	TTG	AGG	CGG	GAT	TTT	TGT	CGT	TTT	AAA	ATC	GGT	579
144	Thr	Leu	Pro	Thr	Phe	Leu	Arq	Arq	Asp	Phe	Cys	Arg	Phe	Lys	Ile	Gly	
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154																	
155						GAT											723
156	Gly	Ph		Thr	Tyr	Asp	Tyr		Arg	His	Phe	Leu		Cys	Cys	Ser	
157			220					225					230				
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159						GAT			-					_	_		771
160	Arg		Phe	GTA	Leu	Asp		GIn	Leu	Lys	Arg	_	Tyr	ITe	Phe	Leu	
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165	250	Tyr	ASII	GTÄ	Arg	255	TTE	GIU	TTE	гÀр	260	пур	MIG	per	GTA	265	
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171	CAA	GTT	CAA	GAA	GTC	CAA	AAA	CGT	TCG	AAG	GAA	ATC	GTG	CTA	CTG	GGA	915
172						Gln											
173				285			-	_	290	•				295		-	
174																	
175	GTT	GAT	GAT	TTG	GAT	ATA	TTC	AAA	GGT	GTG	AAC	TTC	AAG	GTT	TTA	GCG	963
176	Val	Asp	Asp	Leu	Asp	Ile	Phe	Lys	Gly	Val	Asn	Phe	Lys	Val	Leu	Ala	
177			300					305					310				
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179						AAA											1011
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185	330	Val	GIII	116	пеа	335	110	neu	ALG	ALG	340	GIH	rsp	V 4 1	vob	345	
186	550					333					540					0.10	
187	ATC	AAT	GCC	GAG	ATA	AGA	ACA	GTC	TGT	GAA	AGA	ATC	AAT	AAC	GAA	CTG	1107
188						Arg											
189					350				-	355	_				360		
190																	
191						CAG											1155
192	Gly	Ser	Pro	Gly	Tyr	Gln	Pro	Val	Val	Leu	Ile	Asp	Gly	Pro	Val	Ser	
193				365					370					375			
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196	Leu	Ser		Lys	Ala	Ala	Tyr		Ala	Ile	Ala	Asp		Ala	Ile	Val	
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199						GGA											1251
200 201	THE	395	ьeu	Arg	ASD	Gly		ASII	ьeu	тте	PTO	1yr 405	GIU	TYL	val	val	
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211   GCC		мет	Leu	vaı	vaı		GIU	Pne	тте	стА		Ser	Leu	Ser	Leu		GIÀ	
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229																		1587
230		Cys	Met	Asn	Leu	_	Phe	GTÀ	Leu	Asp		Arg	va⊥	Val	Phe		мет	
AGA AGT TTA GCA AGT TGG ATA AAG ATG TCT TGG AAG AAT GCT TAT TCC   1635						510					212					520		
232   Arg Ser Leu Ala Ser Trp Ile Lys Met   Ser Trp Lys Asn Ala Tyr Ser   535	-		3 GM	mm s	<b>aa</b>	3 CIT	maa	3 M 3		» Ma	mam	maa	330	3 3 M	aam	mam	maa	1625
233																		1033
234 235 ATG GCT CAA AAT CGG GCC ATA CTT TTG GAC TAT GAC GGC ACT GTT ACT 236 Met Ala Gln Asn Arg Ala Ile Leu Leu Asp Tyr Asp Gly Thr Val Thr 237 238 239 CCA TCT ATC AGT AAA TCT CCA ACT GAA GCT GTT ACT TCC ATG ATC AAC 240 Pro Ser Ile Ser Lys Ser Pro Thr Glu Ala Val Ile Ser Met Ile Asn 241 555 242 243 AAA CTG TGC AAT GAT CCA AAG AAC ATG GTG TTC ATC GTT AGT GGA CGC 244 Lys Leu Cys Asn Asp Pro Lys Asn Met Val Phe Ile Val Ser Gly Arg 245 570 575 246 247 AGT AGA GAG AAA ATC TTG GCA GTT GGT TCG GCC CGT GTG AGA ACC CGC 248 Ser Arg Glu Lys Ile Leu Ala Val Gly Ser Ala Arg Val Arg Thr Arg 249 590 590 250 251 CAT TGC ACT GAG CAC GGA TAC TTT ATA AGG TGG GCG GGT GAT CAA GAA 253 TGG GAA ACG TGC GCA CGT GAG AAT AAT GTC GGG TGG ATG GAT GAA GAA 253 TGG GAA ACG TGC GCA CGT GAG AAT AAT GTC GGG TGG ATG GAT GAA AAT 256 Trp Glu Thr Cys Ala Arg Glu Asn Asn Val Gly Trp Met Asp Gly Asn 257 TGG GAA ACG TGC GCA CGT GAG AAT AAT GTC GGG TGG ATG GAT GAA AAT 256 Trp Glu Thr Cys Ala Arg Glu Asn Asn Val Gly Trp Met Asp Gly Asn 257 TGG GAA ACG TGC GCA CGT GAG AAT AAT GTC GGG TGG ATG GAT GAA AAT 256 Trp Glu Thr Cys Ala Arg Glu Asn Asn Val Gly Trp Met Asp Gly Asn 257 TGG GAA ACG TGC GCA CGT GAG AAT AAT GTC GGG TGG ATG ATG GAT GAA AAT 256 Trp Glu Thr Cys Ala Arg Glu Asn Asn Val Gly Trp Met Asp Gly Asn 257 TGG GAA ACG TGC GCA CGT GAG AAT AAT GTC GGG TGG TGG ATG GAT GAA AAT 256 Trp Glu Thr Cys Ala Arg Glu Asn Asn Val Gly Trp Met Asp Gly Asn 257 TGG GAA ACG TGC GCA CGT GAG AAT AAT GTC GGG TGG TGG ATG ATG GAA AAT 257 TGG GAA ACG TGC GCA CGT GAG AAT AAT GTC GGG TGG ATG ATG GAA AAT 258 TTP Glu Thr Cys Ala Arg Glu Asn Asn Val Gly Trp Met Asp Gly Asn 257 TGG GAA ACG TGC GCA CGT GAG AAT AAT GTC GGG TGG ATG ATG AAT 258 TTP Glu Thr Cys Ala Arg Glu Asn Asn Val Gly Trp Met Asp Gly Asn 257 TGG GAA ACG TGC GCA CGT GAG AAT AAT GTC GGG TGG ATG ATG AAT 258 TGG GAA ACG TGC GCA CGT GAG AAT AAT GTC GGG TGG ATG ATG ATG ATG ATG ATG ATG ATG		Arg	Set	геп		Set	TIP	тте	цÄг		Set	ırb	пÀР	ASII		ıyı	Ser	
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236		ΔͲα	сст	מא	ል ልጥ	caa	GCC	ΔͲΔ	Сплп	ጥጥር	GAC	ጥልጥ	GAC	GGC	ΔСТ	СПП	ΔСΨ	1683
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239																		
241       555       560       565         242       243       AAA CTG TGC AAT GAT CCA AAG AAC ATG GTG TTC ATC GTT AGT GGA CGC 1779         244       Lys Leu Cys Asn Asp Pro Lys Asn Met Val Phe Ile Val Ser Gly Arg 580       585         245       570       575       575       580       580       585         246       AGT AGA GAG AAA ATC TTG GCA GTT GGT TCG GCG CGT GTG AGA ACC CGC 1827       585       585         248       Ser Arg Glu Lys Ile Leu Ala Val Gly Ser Ala Arg Val Arg Thr Arg 600       595       600         250       CAT TGC ACT GAG CAC GGA TAC TTT ATA AGG TGG GCG GGT GAT CAA GAA 1875         251       CAT TGC ACT GAG CAC GGA TAC TTT ATA AGG TGG GCG GGT GAT CAA GAA 1875         252       His Cys Thr Glu His Gly Tyr Phe Ile Arg Trp Ala Gly Asp Gln Glu 615         253       605       610       610       615         254       625       630       630       630		CCA	TCT	ATC	AGT	AAA	TCT	CCA	ACT	GAA	GCT	GTT	ATC	TCC	ATG	ATC	AAC	1731
242         243       AAA CTG TGC AAT GAT CCA AAG AAC ATG GTG TTC ATC GTT AGT GGA CGC       1779         244       Lys Leu Cys Asn Asp Pro Lys Asn Met Val Phe Ile Val Ser Gly Arg       570       575       580       585         246       570       575       575       580       585       585         246       247       AGT AGA GAG AAA ATC TTG GCA GTT GGT TCG GCG CGT GTG AGA ACC CGC 1827       248       Ser Arg Glu Lys Ile Leu Ala Val Gly Ser Ala Arg Val Arg Thr Arg 590       595       600         250       590       595       600       600         251       CAT TGC ACT GAG CAC GGA TAC TTT ATA AGG TGG GCG GGT GAT CAA GAA 1875       1875         252       His Cys Thr Glu His Gly Tyr Phe Ile Arg Trp Ala Gly Asp Gln Glu 615       605         254       605       605       610       615         254       625       630       630       630	240	Pro	Ser	Ile	Ser	Lys	Ser	Pro	Thr	Glu	Ala	Val	Ile	Ser	Met	Ile	Asn	
243       AAA       CTG       TGC       AAT       GAT       CCA       AAG       AAC       ATG       GTG       TTC       ATC       GTT       AGT       GGA       CGC       1779         244       Lys       Leu       Cys       Asn       Asp       Pro       Lys       Asn       Met       Val       Phe       Ile       Val       Ser       Gly       Arg       Arg       Ses       585	241		555			-		560					565					
244       Lys       Leu       Cys       Asn       Asp       Pro       Lys       Asn       Met       Val       Phe       Ile       Val       Ser       Gly       Arg         245       570       Ser       575       Ser       580       Ser       Ser       Ser       Ser       Ser       AGA       ACC       CGC       1827         246       AGT       AGA       AAA       ATC       TTG       GCA       GTT       GGC       CGT       GTG       AGA       ACC       CGC       1827         248       Ser       Arg       Glu       Lys       Ile       Leu       Ala       Val       GTG       CGT       AGA       ACC       CGC       1827         249       Ser       Arg       Glu       Arg       TTT       ATA       AGG       TGG       GGT       GAT       Arg       Thr       Arg       Arg       TTT       ATA       AGG       TTG       GGT       GAA       ARG       ARA       1875         250       This       Cys       Thr       GI       TTT       ATA       ATT       ATT       ARG       TTG       GGT       GAA       AAT       AAT       <	242																	
245       570       575       580       585         246       247       AGT AGA GAG AAA ATC TTG GCA GTT GGT TCG GCG CGT GTG AGA ACC CGC       1827         248       Ser Arg Glu Lys Ile Leu Ala Val Gly Ser Ala Arg Val Arg Thr Arg       249       590       595       600         250       CAT TGC ACT GAG CAC GGA TAC TTT ATA AGG TGG GCG GGT GAT CAA GAA       1875         252       His Cys Thr Glu His Gly Tyr Phe Ile Arg Trp Ala Gly Asp Gln Glu       615         253       605       605       610       615         254       TGG GAA ACG TGC GCA CGT GAG AAT AAT GTC GGG TGG ATG GAT GGA AAT       1923         255       TGG GAA ACG TGC GCA CGT GAG AAT AAT GTC GGG TGG ATG GAT GGA AAT       1923         256       Trp Glu Thr Cys Ala Arg Glu Asn Asn Val Gly Trp Met Asp Gly Asn       630	243																	1779
246 247	244	Lys	Leu	Cys	Asn	Asp	Pro	Lys	Asn	Met	Val	Phe	Ile	Val	Ser	Gly	Arg	
247 AGT AGA GAG AAA ATC TTG GCA GTT GGT TCG GCG CGT GTG AGA ACC CGC 1827 248 Ser Arg Glu Lys Ile Leu Ala Val Gly Ser Ala Arg Val Arg Thr Arg 249 590 595 600 251 CAT TGC ACT GAG CAC GGA TAC TTT ATA AGG TGG GCG GGT GAT CAA GAA 1875 252 His Cys Thr Glu His Gly Tyr Phe Ile Arg Trp Ala Gly Asp Gln Glu 253 605 610 615 254 255 TGG GAA ACG TGC GCA CGT GAG AAT AAT GTC GGG TGG ATG GAT GGA AAT 1923 256 Trp Glu Thr Cys Ala Arg Glu Asn Asn Val Gly Trp Met Asp Gly Asn 257 620 625 630		570					575					580					585	
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250 251		Ser	Arg	Glu	Lys		Leu	Ala	Val	Gly		Ala	Arg	Val	Arg		Arg	
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252 His Cys Thr Glu His Gly Tyr Phe Ile Arg Trp Ala Gly Asp Gln Glu 253 254 255 TGG GAA ACG TGC GCA CGT GAG AAT AAT GTC GGG TGG ATG GAT GGA AAT 256 Trp Glu Thr Cys Ala Arg Glu Asn Asn Val Gly Trp Met Asp Gly Asn 257 620 625 630		a.m	шол	. am	a.a	a.a	<b>aa</b> .	mag	mmm	3 00 3	3.00	maa	000	aam.	a a m	<b>a</b>	G N N	1075
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254 255 TGG GAA ACG TGC GCA CGT GAG AAT AAT GTC GGG TGG ATG GAT GGA AAT 1923 256 Trp Glu Thr Cys Ala Arg Glu Asn Asn Val Gly Trp Met Asp Gly Asn 257 620 625 630		піѕ	Cys	1111		пта	сту	тАт	File		wrd	ırb	ATG	GTÅ		GTII	GIU	
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### **SEQUENCE VERIFICATION REPORT** PATENT APPLICATION *US/08/779,460B*

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